

1/5

MRAATPLQTVDRPKDWYKTMFKQIHMVHKPDDDTDMYNTPTYTNAGLYNSPYSAQSHPA
 MRAATPLQTVDRPKD YKTMFKQIHMVHKPDDDT MYNTPTYTNAGLYNSPYSAQSHPA
 MRAATPLQTVDRPKD TYKTMFKQIHMVHKPDDDTKMYNTPTYTNAGLYNSPYSAQSHPA

KTQTYRPLSKSHSDNGTDAFKDASSPVPPPHVPPVPLRPRDRSSTEKHDWDPPDRKVD
 KTQTYRPLSKSHSDNGTDAFKDASSPVPPPHVPPVPLRPRDRSSTEKHD DPPDRKVD
 KTQTYRPLSKSHSDNGTDAFKDASSPVPPPHVPPVPLRPRDRSSTEKHDRDPPDRKVD

TRKFRSEPRSI FEYEPGKSSILQHERPVTKPQA-NH₂
 TRKFRSEPRSI FEYEPGKSSILQHERPVTKPQA-NH₂
 TRKFRSEPRSI FEYEPGKSSILQHERPVTKPQA-NH₂

FIG.1

ATGAGAGCAGCAACACCTTTGCAGACAGTTGACCGGCCGAAGGACTGGTACAAGACCATGTTTAAGCAA
 IIII IIII IIIIIIIIIIIIIIIIIII IIIIIII IIIIIIIIIIIIIIIIIII IIIIIIIIIII
 ATGAAAGCAACACACCTTTGCAGACAGTCGACCGGCCGAAGGACTGGTACAAGACGATGTTTAAGCAA

TCCACATGGTGACAAGCCAGATGATGACACAGACATGTATAATACTCCT TATAC
 I IIIIIIIIIIIIIIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIII IIII
 TTCACATGGTGACAAGCCGATGATGACACAGACATGTATAATACTCCTACACCTCACATGAATATAC

ATATAATGCAGGCCTGTACAACCTACAGTGCTCAGTCACATCCTGCTGCCAAGACCCAGACCTAC
 III IIIIIII IIIIIIIII IIIIIIIIIIIIIIIIIIIII IIIIIII IIIIIII IIIII
 ATACAATGCAGGTCTGTACAACCCACCTACAGTGCTCAGTCACACCTGCTGCAAAGACCCAAACCTAC

AGACCCCTCTCCAAAAGCCACTCTGACAATGGCACCAGCGCCTTTAAGGATGCTTCCTCACCTGTCCCTC
 IIIII II IIIIIIIIIIIII IIIII II II I IIIIIIIIIIIII IIIII II II IIII
 AGACCTCTTCCAAAAGCCACTCCGACAACAGCCCAATGCCTTTAAGGATGCGTCCTCCCCAGTGCCTC

CCCCACATGTTCTCTCCAGTCCACCTCTGCGACCAAGAGATCGGTCTTCAACAGAAAAGCATGACTG
 IIIIIIIIIII IIIIIIIIIII II II IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
 CCCCACATGTTCCACCTCCAGTCCCGCGCTTCGACCAAGAGATCGGTCTTCAACAGAAAAGCATGACTG

GGATCCTCCAGACAGAAAAGTGACACGAGAAAATTCGATCGGAGCCACGGTCTATTTTGAATACGAG
 IIIIIIIIIIIIIIIIIIIIIIIII IIIII II I II IIIII II IIIIIIIIIIIIIIIII
 GGATCCTCCAGACAGAAAAGTGACACAAGAAATTCGGGTCTGAGCCAAGGAGTATTTTGAATACGAG

CCTGGGAAGTCATCCATCCTGCAGCACGAACGACCCGTCACGAAACCGCAAGCAGGGCGCCGTAAGGTC
 III IIII I
 CCTGGGAAGTCATCCATCCTGCAGCACGAACGACCCGTCACGAAACCGCAAGCAGGGCGCCGTAAGTCC

FIG.2

2/5

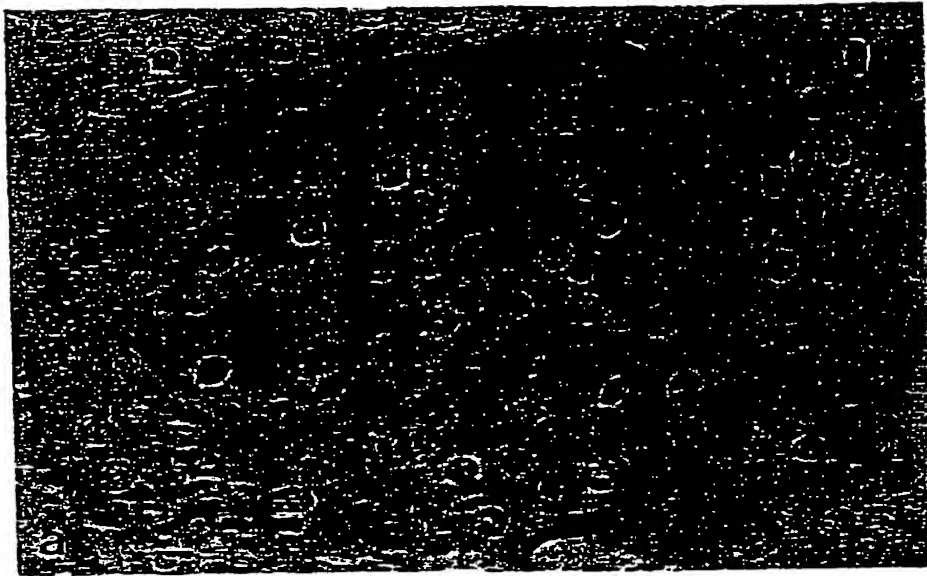
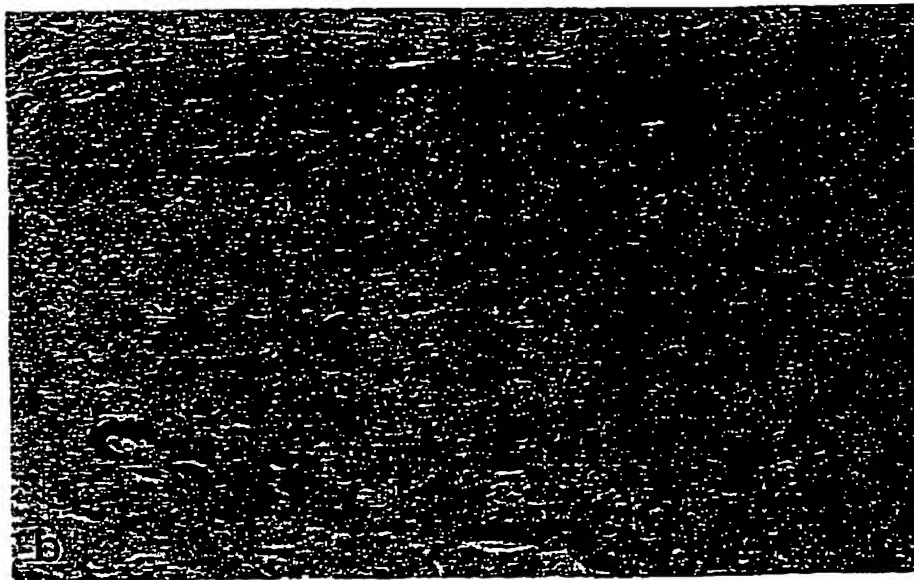
MKATTP LQTVD RPKDWYKTMFKQIHMVHKPDDDTDMYNTPTPHMKYTYNAGLYNPPYSAQ
M+A TPLQTVDRPKDWYKTMFKQIHMVHKPDDDTDMYNTPTPHMKYTYNAGLYN PYS AQ
MRAATPLQTVDRPKDWYKTMFKQIHMVHKPDDDTDMYNTPTPHMKYTYNAGLYNPPYSAQ

SHPAAKTQTYRPLSKSHSDNSPNAFKDASSPVPPPHVPPPVPPPLRPRDRSSTEKHDWDPP
SHPAAKTQTYRPLSKSHSDN +AFKDASSPVPPPHVPPPVPPPLRPRDRSSTEKHDWDPP
SHPAAKTQTYRPLSKSHSDNGTDAFKDASSPVPPPHVPPPVPPPLRPRDRSSTEKHDWDPP

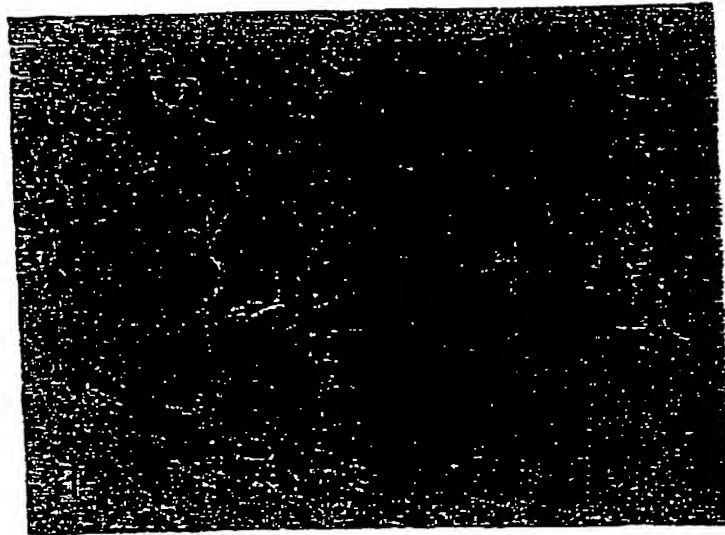
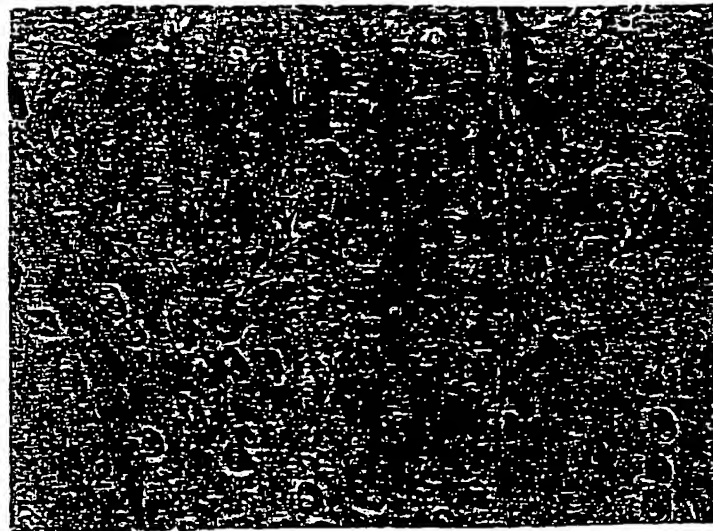
DRKVDTRNFGSEPRSI FEYEPGKSSILQHERPVTKPQA-NH₂
DRKVDTR F SEPRSI FEYEPGKSSILQHERPVTKPQA-NH₂
DRKVDTRKPRSEPRSI FEYEPGKSSILQHERPVTKPQA-NH₂

FIG.3

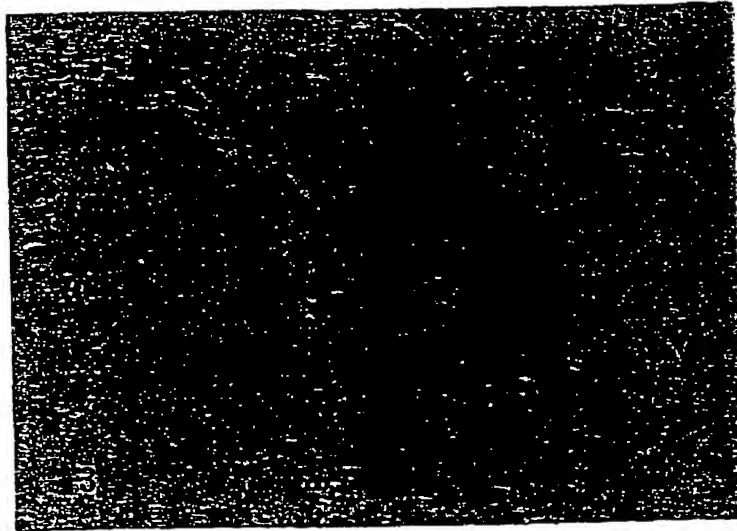
3/5

FIG.4AFIG.4B

4/5

FIG.5AFIG.5B

5/5

FIG.5C